RAW SEQUENCE LISTING DATE: 04/17/2001
PATENT APPLICATION: US/09/202,054 TIME: 11:25:46

Input Set : A:\P1154R2.txt
Output Set: N:\CRF3\04172001\I202054.raw

<110> APPLICANT: Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Mark, Melanie R.
Yang, Ruey-Bing
<120> TITLE OF INVENTION: HUMAN TOLL HOMOLOGUES
<130> FILE REFERENCE: P1154R2
<140> CURRENT APPLICATION NUMBER: US 09/202,054
<141> CURRENT FILING DATE: 1998-12-07
<150> PRIOR APPLICATION NUMBER: PCT/US98/21141
<151> PRIOR FILING DATE: 1998-10-07
<160> NUMBER OF SEQ ID NOS: 32
<210> SEQ ID NO: 1
<211> LENGTH: 1049
<212> TYPE: PRT
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             20                  25                  30
Pro Lys Thr Leu Pro Cys Asp Val Thr Leu Asp Val Pro Lys Asn
         35                  40                  45
His Val Ile Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro
     50                  55                  60
Gly Gly Ile Pro Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn
 65                  70                  75
His Ile Pro Asp Ile Ser Pro Ala Ser Phe His Arg Leu Asp His
             80                  85                  90
Leu Val Glu Ile Asp Phe Arg Cys Asn Cys Val Pro Ile Pro Leu
         95                 100                 105
Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu Gln Ile Lys Pro
    110                 115                 120
Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu Tyr Leu Asp
    125                 130                 135
Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro Ser Leu
    140                 145                 150
Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg Lys
    155                 160                 165
Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly
    170                 175                 180
Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile
    185                 190                 195
Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser
    200                 205                 210
Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser
    215                 220                 225
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```
72  Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile
73                  230                 235                 240
75  Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp
76                  245                 250                 255
78  Leu Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys
79                  260                 265                 270
81  Ala Pro Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala
82                  275                 280                 285
84  Phe Asp Ala Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn
85                  290                 295                 300
87  Ser Leu Gln His Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys
88                  305                 310                 315
90  Leu Gln Glu Leu Asp Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile
91                  320                 325                 330
93  Gly Asp Ala Lys Phe Leu His Phe Leu Pro Ser Leu Ile Gln Leu
94                  335                 340                 345
96  Asp Leu Ser Phe Asn Phe Glu Leu Gln Val Tyr Arg Ala Ser Met
97                  350                 355                 360
99  Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu Lys Ile Leu
100                 365                 370                 375
102  Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe Asn Leu
103                 380                 385                 390
105  Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu Gly
106                 395                 400                 405
108  Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe
109                 410                 415                 420
111  Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro
112                 425                 430                 435
114  Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr
115                 440                 445                 450
117  Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr
118                 455                 460                 465
120  Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys
121                 470                 475                 480
123  Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly
124                 485                 490                 495
126  Gln Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser
127                 500                 505                 510
129  Ser Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser
130                 515                 520                 525
132  Gly Asn Leu Ile Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro
133                 530                 535                 540
135  Leu Ala Glu Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp
136                 545                 550                 555
138  Leu Leu His Ser Thr Ala Phe Glu Glu Leu His Lys Leu Glu Val
139                 560                 565                 570
141  Leu Asp Ile Ser Ser Asn Ser His Tyr Phe Gln Ser Glu Gly Ile
142                 575                 580                 585
144  Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys Val Leu Gln Lys
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```
145                 590                 595                 600
147  Leu Met Met Asn Asp Asn Asp Ile Ser Ser Ser Thr Ser Arg Thr
148                 605                 610                 615
150  Met Glu Ser Glu Ser Leu Arg Thr Leu Glu Phe Arg Gly Asn His
151                 620                 625                 630
153  Leu Asp Val Leu Trp Arg Glu Gly Asp Asn Arg Tyr Leu Gln Leu
154                 635                 640                 645
156  Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn
157                 650                 655                 660
159  Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly Met Pro Pro
160                 665                 670                 675
162  Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys Ser Phe
163                 680                 685                 690
165  Ser Trp Lys Lys Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu Asp
166                 695                 700                 705
168  Leu Ser His Asn Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn
169                 710                 715                 720
171  Cys Ser Arg Ser Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile
172                 725                 730                 735
174  Arg Ser Leu Thr Lys Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg
175                 740                 745                 750
177  Tyr Leu Asp Leu Ser Ser Asn Lys Ile Gln Met Ile Gln Lys Thr
178                 755                 760                 765
180  Ser Phe Pro Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu
181                 770                 775                 780
183  His His Asn Arg Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val
184                 785                 790                 795
186  Trp Trp Val Asn His Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr
187                 800                 805                 810
189  Asp Val Thr Cys Val Gly Pro Gly Ala His Lys Gly Gln Ser Val
190                 815                 820                 825
192  Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp Leu Thr Asn Leu
193                 830                 835                 840
195  Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe Leu Met Val
196                 845                 850                 855
198  Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp Tyr Ile
199                 860                 865                 870
201  Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu Ile
202                 875                 880                 885
204  Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys
205                 890                 895                 900
207  Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys
208                 905                 910                 915
210  Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu
211                 920                 925                 930
213  Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln
214                 935                 940                 945
216  Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys
217                 950                 955                 960
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```
219  Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His
220                  965                 970                 975
222  Gln Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe
223                  980                 985                 990
225  Leu Glu Lys Pro Phe Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys
226                  995                1000                1005
228  Arg Leu Cys Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln
229                 1010                1015                1020
231  Ala His Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Ala Thr
232                 1025                1030                1035
234  Asp Asn His Val Ala Tyr Ser Gln Val Phe Lys Glu Thr Val
235                 1040                1045
237 <210> SEQ ID NO: 2
238 <211> LENGTH: 3283
239 <212> TYPE: DNA
240 <213> ORGANISM: Homo sapiens
242 <400> SEQUENCE: 2
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247  ggacactgaa gagacaaatt cttatccttt ttaacataat cctaatttcc 150
249  aaactccttg gggctagatg gtttcctaaa actctgccct gtgatgtcac 200
251  tctggatgtt ccaaagaacc atgtgatcgt ggactgcaca gacaagcatt 250
253  tgacagaaat tcctggaggt attcccacga acaccacgaa cctcaccctc 300
255  accattaacc acataccaga catctcccca gcgtcctttc acagactgga 350
257  ccatctggta gagatcgatt tcagatgcaa ctgtgtacct attccactgg 400
259  ggtcaaaaaa caacatgtgc atcaagaggc tgcagattaa acccagaagc 450
261  tttagtggac tcacttattt aaaatccctt tacctggatg gaaaccagct 500
263  actagagata ccgcagggcc tcccgcctag cttacagctt ctcagccttg 550
265  aggccaacaa catcttttcc atcagaaaag agaatctaac agaactggcc 600
267  aacatagaaa tactctacct gggccaaaac tgttattatc gaaatccttg 650
269  ttatgtttca tattcaatag agaaagatgc cttcctaaac ttgacaaagt 700
271  taaaagtgct ctccctgaaa gataacaatg tcacagccgt ccctactgtt 750
273  ttgccatcta ctttaacaga actatatctc tacaacaaca tgattgcaaa 800
275  aatccaagaa gatgatttta ataacctcaa ccaattacaa attcttgacc 850
277  taagtggaaa ttgccctcgt tgttataatg ccccatttcc ttgtgcgccg 900
279  tgtaaaaata attctcccct acagatccct gtaaatgctt ttgatgcgct 950
281  gacagaatta aaagttttac gtctacacag taactctctt cagcatgtgc 1000
283  ccccaagatg gtttaagaac atcaacaaac tccaggaact ggatctgtcc 1050
285  caaaacttct tggccaaaga aattggggat gctaaatttc tgcattttct 1100
287  ccccagcctc atccaattgg atctgtcttt caattttgaa cttcaggtct 1150
289  atcgtgcatc tatgaatcta tcacaagcat tttcttcact gaaaagcctg 1200
291  aaaattctgc ggatcagagg atatgtcttt aaagagttga aaagctttaa 1250
293  cctctcgcca ttacataatc ttcaaaatct tgaagttctt gatcttggca 1300
295  ctaactttat aaaaattgct aacctcagca tgtttaaaca atttaaaaga 1350
297  ctgaaagtca tagatctttc agtgaataaa atatcacctt caggagattc 1400
299  aagtgaagtt ggcttctgct caaatgccag aacttctgta gaaagttatg 1450
301  aaccccaggt cctggaacaa ttacattatt tcagatatga taagtatgca 1500
303  aggagttgca gattcaaaaa caaagaggct tctttcatgt ctgttaatga 1550
305  aagctgctac aagtatgggc agaccttgga tctaagtaaa aatagtatat 1600
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309  aatctgtcag gaaatctcat tagccaaact cttaatggca gtgaattcca 1700
311  acctttagca gagctgagat atttggactt ctccaacaac cggcttgatt 1750
313  tactccattc aacagcattt gaagagcttc acaaactgga agttctggat 1800
315  ataagcagta atagccatta ttttcaatca gaaggaatta ctcatatgct 1850
317  aaactttacc aagaacctaa aggttctgca gaaactgatg atgaacgaca 1900
319  atgacatctc ttcctccacc agcaggacca tggagagtga gtctcttaga 1950
321  actctggaat tcagaggaaa tcacttagat gttttatgga gagaaggtga 2000
323  taacagatac ttacaattat tcaagaatct gctaaaatta gaggaattag 2050
325  acatctctaa aaattcccta agtttcttgc cttctggagt ttttgatggt 2100
327  atgcctccaa atctaaagaa tctctctttg gccaaaaatg ggctcaaatc 2150
329  tttcagttgg aagaaactcc agtgtctaaa gaacctggaa actttggacc 2200
331  tcagccacaa ccaactgacc actgtccctg agagattatc caactgttcc 2250
333  agaagcctca agaatctgat tcttaagaat aatcaaatca ggagtctgac 2300
335  gaagtatttt ctacaagatg ccttccagtt gcgatatctg gatctcagct 2350
337  caaataaaat ccagatgatc caaaagacca gcttcccaga aaatgtcctc 2400
339  aacaatctga agatgttgct tttgcatcat aatcggtttc tgtgcacctg 2450
341  tgatgctgtg tggtttgtct ggtgggttaa ccatacggag gtgactattc 2500
343  cttacctggc cacagatgtg acttgtgtgg ggccaggagc acacaagggc 2550
345  caaagtgtga tctccctgga tctgtacacc tgtgagttag atctgactaa 2600
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359  tctggaaaac ctttcccaga gcatacagct tagcaaaaag acagtgtttg 2950
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363  ttgtcccatc agaggctcat ggatgaaaaa gttgatgtga ttatcttgat 3050
365  atttcttgag aagccctttc agaagtccaa gttcctccag ctccggaaaa 3100
367  ggctctgtgg gagttctgtc cttgagtggc caacaaaccc gcaagctcac 3150
369  ccatacttct ggcagtgtct aaagaacgcc ctggccacag acaatcatgt 3200
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373  acaactgcct agtttaccaa ggagaggcct ggc 3283
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376 <211> LENGTH: 1041
377 <212> TYPE: PRT
378 <213> ORGANISM: Homo sapiens
380 <400> SEQUENCE: 3
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384  Leu Leu Ile Ser Gly Ser Cys Glu Leu Cys Ala Glu Glu Asn Phe
385                20                  25                  30
387  Ser Arg Ser Tyr Pro Cys Asp Glu Lys Lys Gln Asn Asp Ser Val
388                35                  40                  45
390  Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val Pro Gln Thr
391                50                  55                  60
393  Val Gly Lys Tyr Val Thr Glu Leu Asp Leu Ser Asp Asn Phe Ile
394                65                  70                  75
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